

FIGURE 1

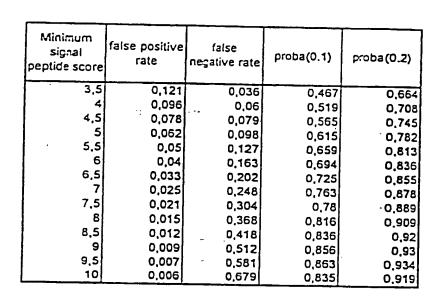
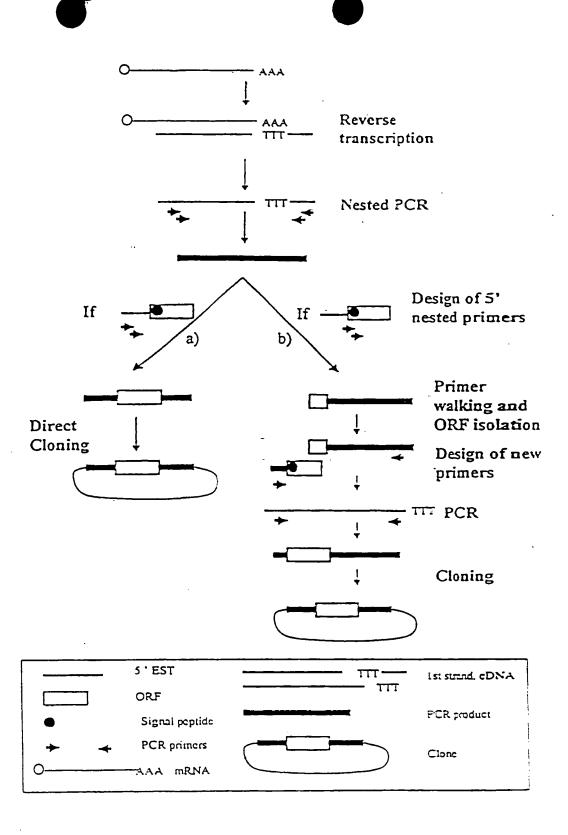
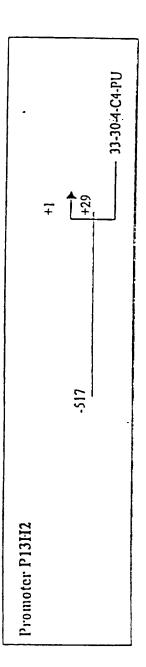


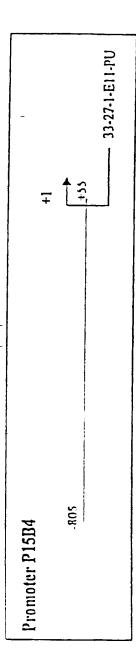
FIGURE 2



## figure 3

Description of promoters structure isolated from SignalTag 5'ESTs





	- ÎŞ	33-464-F4-PU
	-500	
Promoter P29B6		

## FIGURE 4

Description of Transcription Factor Binding Sites present in promoters isolated from SignalTag sequences

Promoter caniones D12	H2 (546 bp)	:				
<del>-</del>	Position	Orientation	Score	Length	Sequence	Location in:
				Ü	-	SEQ ID NO: 17
CMYB 01	-502	+	0.983	9	TGTCAGTTG	17-25
	-501	-	0.961	10	CCCAACTGAC	complement of 18-27
	-444	-	0.960	11	AATAGAATTAG	complement of 75-85
	-425	+	0.966	11		94-104
	-390	-	0.960	11	GCACACCTCAG	complement of 129-139
GATA C	-364	-	0.964	11		complement of 155-165
CMYB_01	-349	+	0.958	9	CTTCAGTTG	170-178 176-189
GATA1_02	-343	+	0.959	14	TIGIAGATAGGACA	176-189 180-190
GATA_C	-339	+	0.953	11	AUA I AUGACAT	180-190 284-299
TAL1ĀLPHAE47_01	-235	+	0.973		CATALOLOGICATO	284-299 284-299
TAL1BETAE47_01	-235	+	0.983		CATAACACATCCTAAC	284-299 284 <b>-</b> 299
TAL1BETAITF2_01	-235	+			CATAACAGATGGTAAG	complement of 287-296
MYOD_Q6	-232	-			TOAACATAAACTA	complement of 302-314
GATA1_04	-217	<del>-</del>			ACTTCCCA ATTCC	393-405
IK1 <b>0</b> 1	-126	+			AULIUUUAALIUU ACTTCCCA ATTC	393-405 393-404
IK2 <b>_0</b> 1	-126	+				393-404 396-405
CREL 01	-123	+				423-436
GATAI_02		+				complement of 478-489
SRY 02	-41 22	-				486-493
E2F_02		+				complement of 514-521
MZF1_01	-5	-	0.975	ō	TOMOGOUN	
<b>D</b>	5D4 (0/4 * )	١٠				
rromoter sequence P1	Doction Doct	Orientation	Score	Lenoth	Sequence	Location in:
MATATLIX	TOSTITOT	C. ICHIAUUH			-	SEQ ID NO: 20
NEV O6	-748	-	0.956	11	GGACCAATCAT	complement of 60-70
MZFI 01	-748 -738	+	0.962	8	CCTGGGGA	70 <b>-</b> 77 -
CMYR 01	-738 -684	+	0.994	9	TGACCGTTG	124-132
VMYR 02	-682	· -	0.985	9	TCCAACGGT	complement of 126-134
STAT 01	-673	+	0.968	9	TTCCTGGAA	135-143
STAT 01	-673	· -	0.951	9	TTCCAGGAA	complement of 135-143
<b></b>	-556	-	0.956	8	TTGGGGGA	complement of 252-259
	-451	+	0.965	12	GAATGGGATTTC	357-368 384-301
MZF1_01	-424	+	0.986	8	AGAGGGA	384-391 complement of 410-421
SRY_02	-398	-	0.955	12	GAAAACAAAACA	
MZF1_01	-216	+	0.960	8		592 <b>-</b> 599 618-6 <b>2</b> 7
MYOD_Q6	-190	+	0.981	10	AUCATUTUCU TOCCA COTTOC	618-627 632-642
DELTAEF1_01	-176	+	0.958		CACCCA ATTAT	632-642 complement of 813-823
S8_ <b>0</b> 1	5	-		_	VAUVLAATTAT AGAGGGGA	complement of 824-831
M <b>ZF1</b> _01	16	-	0.986	8	AUUUUUAUA	complement of 024-031
_	10DC (555	2).				
	Docition	P): Orientation	Score	Lenoth	Sequence	Location in:
MIZUTIX	r osition	Or tentanon	DEUI C	~~g.11	<del>-</del>	<b>SEQ ID NO: 23</b>
ARNT OI	-311	+	0.964	16	GGACTCACGTGCTGCT	191-206
ARNT 01		+ +	0.965	. 12	ACTCACGTGCTG	193-204
	" <b>4U</b> O	→	J. J. U.J		A COTTO A COTTO COTTO	
NMYC_01	-309 -309	+ +	0.985	12	ACTCACGTGCTG	193-204
NMYC_01 USF_01	-309			12	CAGCACGTGAGT	complement of 193-204
NMYC_01 USF_01 USF_01	-309 -309	+	0.985	12 12	CAGCACGTGAGT CAGCACGTGAGT	complement of 193-204 complement of 193-204
NMYC_01 USF_01 USF_01 NMYC_01	-309 -309 -309	÷ -	0.985 0.985	12 12 12	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT	complement of 193-204 complement of 193-204 complement of 193-204
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02	-309 -309 -309 -309	÷ -	0.985 0.985 0.956	12 12 12 8	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC	complement of 193-204 complement of 193-204 complement of 193-204 195-202
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C	-309 -309 -309 -309 -307	+ - - -	0.985 0.985 0.956 0.972	12 12 12 8 8	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C	-309 -309 -309 -309 -307 -307	+ - - -	0.985 0.985 0.956 0.972 0.997 0.991 0.968	12 12 12 8 8	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01	-309 -309 -309 -309 -307	÷ - - + -	0.985 0.985 0.956 0.972 0.997 0.991 0.968 0.963	12 12 12 8 8 8 8	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01 ELK1_02	-309 -309 -309 -309 -307 -307 -292	÷ - - + -	0.985 0.985 0.956 0.972 0.997 0.991 0.968 0.963	12 12 12 8 8 8 8 14 10	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT TCCGGAAGCC	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410 400-409
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01 ELK1_02 CETS1P54_01	-309 -309 -309 -307 -307 -307 -292 -105 -102 -42	+ - - - + - -	0.985 0.985 0.956 0.972 0.997 0.991 0.968 0.963 0.974	12 12 12 8 8 8 14 10	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT TCCGGAAGCC AGTGACTGAAC	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410 400-409 complement of 460-470
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01 ELK1_02 CETSIP54_01 AP1_Q4	-309 -309 -309 -307 -307 -307 -292 -105 -102 -42 -42	+ - - - + - -	0.985 0.985 0.956 0.972 0.997 0.991 0.968 0.963 0.974 0.963	12 12 12 8 8 8 14 10 11	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT TCCGGAAGCC AGTGACTGAAC AGTGACTGAAC	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410 400-409 complement of 460-470 complement of 460-470
NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01 ELK1_02 CETS1P54_01	-309 -309 -309 -307 -307 -307 -292 -105 -102 -42	+ - - - + - -	0.985 0.985 0.956 0.972 0.997 0.991 0.968 0.963 0.974	12 12 12 8 8 8 14 10 11	CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT TCCGGAAGCC AGTGACTGAAC	complement of 193-204 complement of 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410 400-409 complement of 460-470
	CMYB_01 MYOD_Q6 S8_01 S8_01 DELTAEF1_01 GATA_C CMYB_01 GATAI_02 GATA_C TAL1ALPHAE47_01 TAL1BETAE47_01 TAL1BETAET2_01 MYOD_Q6 GATAI_04 IK1_01 IK2_01 CREL_01 GATAI_02 SRY_02 E2F_02 MZF1_01  Promoter sequence P1 Matrix  NFY_Q6 MZF1_01 CMYB_01 VMYB_02 STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 IK2_01 MZF1_01 STAT_01 MZF1_01 STAT_01 MZF1_01 SRY_02 MZF1_01 SRY_02 MZF1_01 Promoter sequence P1 M3EF1_01 SRY_02 MZF1_01 MZF1_01 Promoter sequence P1 M3EF1_01 SRY_02 MZF1_01 MZF1_01 Promoter sequence P1 M3EF1_01	Matrix Position  CMYB_01 -502 MYOD_Q6 -501 S8_01 -444 S8_01 -425 DELTAEF1_01 -390 GATA_C -364 CMYB_01 -349 GATA1_02 -343 GATA_C -339 TAL1ALPHAE47_01 -235 TAL1BETAEF1_01 -235 TAL1BETAITF2_01 -235 MYOD_Q6 -232 GATA1_04 -217 IK1_01 -126 IK2_01 -126 CREL_01 -123 GATA1_02 -96 SRY_02 -41 E2F_02 -33 MZF1_01 -5  Promoter sequence P15B4 (861 bp) Matrix Position  NFY_Q6 -748 MZF1_01 -684 VMYB_01 -684 VMYB_02 -682 STAT_01 -673 STAT_01 -673 STAT_01 -673 STAT_01 -673 MZF1_01 -556 IK2_01 -451 MZF1_01 -556 IK2_01 -451 MZF1_01 -216 MYOD_Q6 -190 DELTAEF1_01 -216 MYOD_Q6 -190 DELTAEF1_01 -176 S8_01 -5 MZF1_01 -176 S8_01 -176 S	CMYB 01	Matrix         Position         Orientation         Score           CMYB 01         -502         +         0.983           MYOD_Q6         -501         -         0.960           S8 01         -444         -         0.960           S8 01         -425         +         0.966           DELTAEF1_01         -390         -         0.960           GATA_C         -364         -         0.964           CMYB 01         -349         +         0.958           GATA_O2         -343         +         0.959           GATA_C         -339         +         0.953           TAL1ALPHAE47_01         -235         +         0.973           TAL1BETAE47_01         -235         +         0.973           TAL1BETAITF2_01         -235         +         0.978           MYOD_Q6         -232         -         0.954           GATA1_04         -217         -         0.953           IK1_01         -126         +         0.963           IK2_01         -126         +         0.965           CREL_01         -123         +         0.962           GATA1_02         -96 <t< td=""><td>Matrix         Position         Orientation         Score         Length           CMYB_01         -502         +         0.983         9           MYOD_06         -501         -         0.961         10           S8_01         -4444         -         0.960         11           S8_01         -425         +         0.966         11           DELTAEF1_01         -390         -         0.964         11           GATA_C         -364         -         0.964         11           CMYB_01         -349         +         0.958         9           GATA_I_02         -343         +         0.958         9           GATA_I_02         -343         +         0.953         11           TAL1BETAE47_01         -235         +         0.973         16           MYOD_Q6         -232         -         0.954         10           GATAI_04         -217         -         0.953         13           IK1_01         -126         +         0.963         13           IK2_01         -126         +         0.963         12           CREL_01         -126         +         0.955</td><td>  Matrix</td></t<>	Matrix         Position         Orientation         Score         Length           CMYB_01         -502         +         0.983         9           MYOD_06         -501         -         0.961         10           S8_01         -4444         -         0.960         11           S8_01         -425         +         0.966         11           DELTAEF1_01         -390         -         0.964         11           GATA_C         -364         -         0.964         11           CMYB_01         -349         +         0.958         9           GATA_I_02         -343         +         0.958         9           GATA_I_02         -343         +         0.953         11           TAL1BETAE47_01         -235         +         0.973         16           MYOD_Q6         -232         -         0.954         10           GATAI_04         -217         -         0.953         13           IK1_01         -126         +         0.963         13           IK2_01         -126         +         0.963         12           CREL_01         -126         +         0.955	Matrix